re-run

RAW SEQUENCE LISTING   DATE: 10/01/2004
PATENT APPLICATION: **US/09/894,030**   TIME: 10:40:54

Input Set : **A:\PTO_VSK.txt**
Output Set: **N:\CRF4\10012004\I894030.raw**

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    2 <110> APPLICANT: Hansen, J. Norman
    4 <120> TITLE OF INVENTION: Construction of a Structural Variant of Sublancin to
Facilitate its
    5         Isolation and Use in Bioremediation of Environmental Contamination by Gram-
    6         positive Spore Formers such as Bacillus anthrasis
    8 <130> FILE REFERENCE: 108172-00058
C-->   10 <140> CURRENT APPLICATION NUMBER: US/09/894,030
C-->   10 <141> CURRENT FILING DATE: 2001-06-29
   10 <150> PRIOR APPLICATION NUMBER: 60/215,449
   11 <151> PRIOR FILING DATE: 2000-06-29
   13 <160> NUMBER OF SEQ ID NOS: 3
   15 <170> SOFTWARE: PatentIn version 3.1
   17 <210> SEQ ID NO: 1
   18 <211> LENGTH: 2517
   19 <212> TYPE: DNA
   20 <213> ORGANISM: Artificial Sequence
   22 <220> FEATURE:
   23 <223> OTHER INFORMATION: EcoRI-HindIII insert of the pLPVc intregrative plasmid.
   25 <400> SEQUENCE: 1
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   28 tcaacgagct ggattaacag gtgggcataa gagttaagat aaatttaaac ttatataaca       120
   30 catcgcttaa agtttttttg ttttaaaaac ttaaaaaaca tggtaaaatt atataaaaac       180
   32 ataagaaaga gtgattatat ggaatatgta gttatgataa tcattttatt agcacttttc       240
   34 tttattttta ctgttttcct aaatacacgt tatagttttg atgaaaaatg cttagtctta       300
   36 aaatttggtt tatctaaaac agaaattcca attaatcaaa tagttagtat taaagagtca       360
   38 gacaagtatg gagttgcaga taatatcgat tataaaattg gtatgccata tgctcaacca       420
   40 gatagaattg ttattgaaac tacaaataag cgttttctag tttttttaaa tggagctcaa       480
   42 caatttattc aaaagtataa aagggttagt gtttgaacat aaaaaagtac cttcttacaa       540
   44 tagaaggtac ttttttgtat ctataattat taaaaattta cctaaatttt tatcattatt       600
   46 aattcaaaat aaatccataa tagtcaattt tatttagtgt attacaacca attcggatcc       660
   48 aagcacccat tagttcaaca aacgaaaatt ggataaagtg ggatatttt aaaatatata        720
   50 tttatgttac agtaatattg acttttaaaa aaggattgat tctaatgaag aaagcagaca       780
   52 agtaagcctc ctaaattcac tttagataaa aatttaggag gcatatcaaa tgaactttaa       840
   54 taaaattgat ttagacaatt ggaagagaaa agagatattt aatcattatt tgaaccaaca       900
   56 aacgactttt agtataacca cagaaattga tattagtgtt ttataccgaa acataaaaca       960
   58 agaaggatat aaattttacc ctgcatttat tttcttagtg acaagggtga taaactcaaa      1020
   60 tacagctttt agaactggtt acaatagcga cggagagtta ggttattggg ataagttaga      1080
   62 gccactttat acaatttttg atggtgtatc taaaacattc tctggtattt ggactcctgt      1140
   64 aaagaatgac ttcaaagagt tttatgattt ataccttct gatgtagaga aatataatgg       1200
   66 ttcggggaaa ttgtttccca aaacacctat acctgaaaat gcttttctc tttctattat       1260
   68 tccatggact tcatttactg ggtttaactt aaatatcaat aataatagta attaccttct      1320
   70 acccattatt acagcaggaa aattcattaa taaaggtaat tcaatatatt taccgctatc      1380
   72 tttacaggta catcattctg tttgtgatgg ttatcatgca ggattgttta tgaactctat      1440
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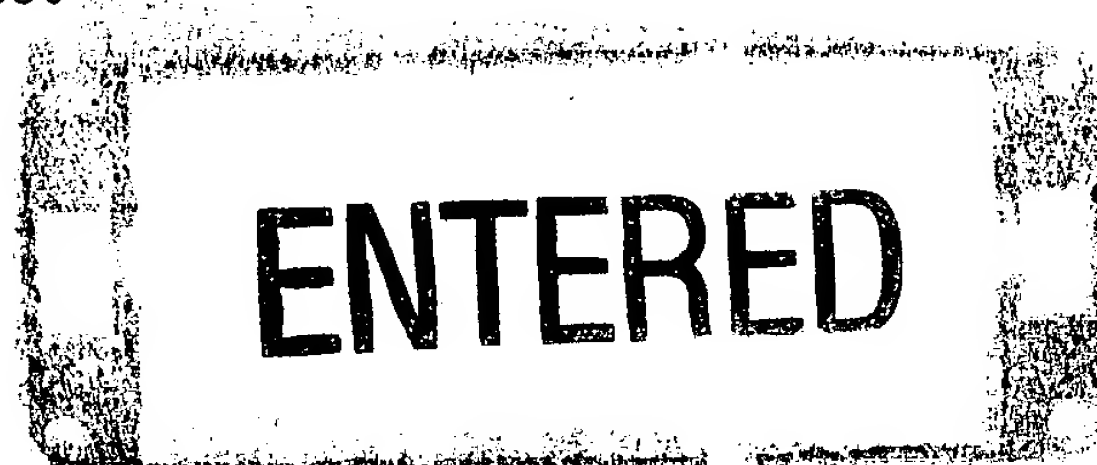
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 76 actttttaca gtcggttttc taatgtcact aacctgcccc gttagttgaa gaagggattc   1560
 78 gtgtattaca accaattctg tttattgata ggtaataaag ttttttttct atgatttatg   1620
 80 aacaagtttc cttataattt tcaaaaaaaa ataaaaaata tggttgaatt tagatttatc   1680
 82 ttcctttata ttaaaaaatg taatccggat tgcaaacaaa tggggaggtt ttacaaatgg   1740
 84 aaaagctatt taaagaagtt aaactcgagg aactcgaaaa ccaaaaaggt agtggattag   1800
 86 gaaaagctca gtgtgctgcg ttgtggctac aatgtgctag tggcggtaca attggttgtg   1860
 88 gtggcggagc tgttgcttgt caaaactatc gtcaattctg cagataaaac atttgtagag   1920
 90 ggaatatttt aaatattccc tcatatttaa agcggggatt gaaattgaat aagaaaaaga   1980
 92 aatatgttca tactaaacag tttaatagtc atgattgtgg actagcttgt atctcgtcaa   2040
 94 ttttaaagtt tcataacctt aactatggaa ttgatttctt actagaccta attggggata   2100
 96 aggaaggcta tagtttaaga gacttaattg ttatttttaa gaagatgggg ataaaaacta   2160
 98 ggccacttga attgcaagaa aataagacat tcgaagccct aaaacaaata aagctccctt   2220
100 gtatagcttt gttagaaggg gaggaatatg gacattacat aacaatatac gaaattagaa   2280
102 ataactattt acttgttagt gatcctgata aagacaaaat aactaaaata aaaaaagagg   2340
104 attttgaaag taaattcaca aactttatat tagaaattga caaagagtca attcctgaaa   2400
106 aagaaaaaga tcaaaaaaaa cattcttact tttttaagga catacttttt agaaataaat   2460
108 tgatcgtttt tgtgattta ttgacttcct tgttcgttgt gggtcttgct gaagctt      2517
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116 <211> LENGTH: 300
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: The sublancin-His Tag gene and its corresponding peptide
sequence.
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (1)..(300)
126 <223> OTHER INFORMATION:
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130 atg gaa aag cta ttt aaa gaa gtt aaa ctc gag gaa ctc gaa aac caa        48
131 Met Glu Lys Leu Phe Lys Glu Val Lys Leu Glu Glu Leu Glu Asn Gln
132 1               5                   10                  15
134 aaa ggt agt gga tta gga aaa gct cag tgt gct gcg ttg tgg cta caa        96
135 Lys Gly Ser Gly Leu Gly Lys Ala Gln Cys Ala Ala Leu Trp Leu Gln
136             20                  25                  30
138 tgt gct agt ggc ggt aca att ggt tgt ggt ggc ggc gcc gtt gct tgt       144
139 Cys Ala Ser Gly Gly Thr Ile Gly Cys Gly Gly Gly Ala Val Ala Cys
140         35                  40                  45
142 caa aac tat cgt caa ttc tgt aga ggt ggt ggt ggg gga ggc ggg gga      192
143 Gln Asn Tyr Arg Gln Phe Cys Arg Gly Gly Gly Gly Gly Gly Gly Gly
144     50                  55                  60
146 ggg ggt ggt ggt gga gga ggt ggt ggt ggt ggt ggt atg tca aag ttc      240
147 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Met Ser Lys Phe
148 65                  70                  75                  80
150 gat gat ttc gat cta gat gtt gtg aaa gtc tct aaa caa gac tca aaa      288
151 Asp Asp Phe Asp Leu Asp Val Val Lys Val Ser Lys Gln Asp Ser Lys
152             85                  90                  95
154 atc act ccg caa                                                      300
155 Ile Thr Pro Gln
156             100
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159 <210> SEQ ID NO: 3
160 <211> LENGTH: 100
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: The peptide sequence for sublancin-His Tag.
167 <400> SEQUENCE: 3
169 Met Glu Lys Leu Phe Lys Glu Val Lys Leu Glu Glu Leu Glu Asn Gln
170 1               5                   10                  15
173 Lys Gly Ser Gly Leu Gly Lys Ala Gln Cys Ala Ala Leu Trp Leu Gln
174             20                  25                  30
177 Cys Ala Ser Gly Gly Thr Ile Gly Cys Gly Gly Gly Ala Val Ala Cys
178         35                  40                  45
181 Gln Asn Tyr Arg Gln Phe Cys Arg Gly Gly Gly Gly Gly Gly Gly Gly
182     50                  55                  60
185 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Met Ser Lys Phe
186 65                  70                  75                  80
189 Asp Asp Phe Asp Leu Asp Val Val Lys Val Ser Lys Gln Asp Ser Lys
190             85                  90                  95
193 Ile Thr Pro Gln
194             100
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:129 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:126